

# SEQUENCE LISTING

<110> GARGER, Stephen A.  
 TURPEN, Thomas H.  
 KUMAGAI, Monto H.

<120> PRODUCTION OF LYSOSOMAL ENZYMES IN  
 PLANTS BY TRANSIENT EXPRESSION

<130> 008010087CPUS06

<140> To Be Assigned

<141> 2001-11-13

<160> 37

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 15

<212> PRT

<213> Rice

<400> 1

Ser	Asn	Leu	Thr	Ala	Gly	Met	Leu	Asp	Asn	Gly	Leu	Ala	Arg	Thr
1				5					10				15	

<210> 2

<211> 15

<212> PRT

<213> Homo sapiens

<400> 2

Asp	Ile	Pro	Gly	Ala	Arg	Ala	Leu	Asp	Asn	Gly	Leu	Ala	Arg	Thr
1				5					10				15	

<210> 3

<211> 1290

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1290)

<400> 3

atg	cag	ctg	agg	aac	cca	gaa	cta	cat	ctg	ggc	tgc	gcg	ctt	gcg	ctt	48
Met	Gln	Leu	Arg	Asn	Pro	Glu	Leu	His	Leu	Gly	Cys	Ala	Leu	Ala	Leu	
1				5					10				15			

cgc	ttc	ctg	gcc	ctc	gtt	tcc	tgg	gac	atc	cct	ggg	gct	aga	gca	ctg	96
Arg	Phe	Leu	Ala	Leu	Val	Ser	Trp	Asp	Ile	Pro	Gly	Ala	Arg	Ala	Leu	



agt atc ttg gac tgg aca tct ttt aac cag gag aga att gtt gat gtt	768
Ser Ile Leu Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val	
245 250 255	
gct gga cca ggg ggt tgg aat gac cca gat atg tta gtg att ggc aac	816
Ala Gly Pro Gly Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn	
260 265 270	
ttt ggc ctc agc tgg aat cag caa gta act cag atg gcc ctc tgg gct	864
Phe Gly Leu Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala	
275 280 285	
atc atg gct gct cct tta ttc atg tct aat gac ctc cga cac atc agc	912
Ile Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser	
290 295 300	
cct caa gcc aaa gct ctc ctt cag gat aag gac gta att gcc atc aat	960
Pro Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn	
305 310 315 320	
cag gac ccc ttg ggc aag caa ggg tac cag ctt aga cag gga gac aac	1008
Gln Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn	
325 330 335	
ttt gaa gtg tgg gaa cga cct ctc tca ggc tta gcc tgg gct gta gct	1056
Phe Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala	
340 345 350	
atg ata aac cgg cag gag att ggt gga cct cgc tct tat acc atc gca	1104
Met Ile Asn Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala	
355 360 365	
gtt gct tcc ctg ggt aaa gga gtg gcc tgt aat cct gcc tgc ttc atc	1152
Val Ala Ser Leu Gly Lys Gly Val Ala Cys Asn Pro Ala Cys Phe Ile	
370 375 380	
aca cag ctc ctc cct gtg aaa agg aag cta ggg ttc tat gaa tgg act	1200
Thr Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr	
385 390 395 400	
tca agg tta aga agt cac ata aat ccc aca ggc act gtt ttg ctt cag	1248
Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu Gln	
405 410 415	
cta gaa aac aca atg cag atg tct tta aaa gac tta ctt taa	1290
Leu Glu Asn Thr Met Gln Met Ser Leu Lys Asp Leu Leu *	
420 425	

<210> 4  
 <211> 428  
 <212> PRT  
 <213> Homo sapiens



420

425

<210> 5  
 <211> 1308  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(1308)

&lt;400&gt; 5

atg cag ctg agg aac cca gaa cta cat ctg ggc tgc gcg ctt gcg ctt	48
Met Gln Leu Arg Asn Pro Glu Leu His Leu Gly Cys Ala Leu Ala Leu	
1 5 10 15	
cgc ttc ctg gcc ctc gtt tcc tgg gac atc cct ggg gct aga gca ctg	96
Arg Phe Leu Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu	
20 25 30	
gac aat gga ttg gca agg acg cct acc atg ggc tgg ctg cac tgg gag	144
Asp Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu	
35 40 45	
cgc ttc atg tgc aac ctt gac tgc cag gaa gag cca gat tcc tgc atc	192
Arg Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile	
50 55 60	
agt gag aag ctc ttc atg gag atg gca gag ctc atg gtc tca gaa ggc	240
Ser Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly	
65 70 75 80	
tgg aag gat gca ggt tat gag tac ctc tgc att gat gac tgt tgg atg	288
Trp Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met	
85 90 95	
gct ccc caa aga gat tca gaa ggc aga ctt cag gca gac cct cag cgc	336
Ala Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg	
100 105 110	
ttt cct cat ggg att cgc cag cta gct aat tat gtt cac agc aaa gga	384
Phe Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly	
115 120 125	
ctg aag cta ggg att tat gca gat gtt gga aat aaa acc tgc gca ggc	432
Leu Lys Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly	
130 135 140	
ttc cct ggg agt ttt gga tac tac gac att gat gcc cag acc ttt gct	480
Phe Pro Gly Ser Phe Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala	
145 150 155 160	
gac tgg gga gta gat ctg cta aaa ttt gat ggt tgt tac tgt gac agt	528
Asp Trp Gly Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser	

165										170					175					
ttg gaa aat ttg gca gat ggt tat aag cac atg tcc ttg gcc ctg aat	576																			
Leu Glu Asn Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn																				
180 185 190																				
agg act ggc aga agc att gtg tac tcc tgt gag tgg cct ctt tat atg	624																			
Arg Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met																				
195 200 205																				
tgg ccc ttt caa aag ccc aat tat aca gaa atc cga cag tac tgc aat	672																			
Trp Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn																				
210 215 220																				
cac tgg cga aat ttt gct gac att gat gat tcc tgg aaa agt ata aag	720																			
His Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys																				
225 230 235 240																				
agt atc ttg gac tgg aca tct ttt aac cag gag aga att gtt gat gtt	768																			
Ser Ile Leu Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val																				
245 250 255																				
gct gga cca ggg ggt tgg aat gac cca gat atg tta gtg att ggc aac	816																			
Ala Gly Pro Gly Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn																				
260 265 270																				
ttt ggc ctc agc tgg aat cag caa gta act cag atg gcc ctc tgg gct	864																			
Phe Gly Leu Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala																				
275 280 285																				
atc atg gct gct cct tta ttc atg tct aat gac ctc cga cac atc agc	912																			
Ile Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser																				
290 295 300																				
cct caa gcc aaa gct ctc ctt cag gat aag gac gta att gcc atc aat	960																			
Pro Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn																				
305 310 315 320																				
cag gac ccc ttg ggc aag caa ggg tac cag ctt aga cag gga gac aac	1008																			
Gln Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn																				
325 330 335																				
ttt gaa gtg tgg gaa cga cct ctc tca ggc tta gcc tgg gct gta gct	1056																			
Phe Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala																				
340 345 350																				
atg ata aac cgg cag gag att ggt gga cct cgc tct tat acc atc gca	1104																			
Met Ile Asn Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala																				
355 360 365																				
gtt gct tcc ctg ggt aaa gga gtg gcc tgt aat cct gcc tgc ttc atc	1152																			
Val Ala Ser Leu Gly Lys Gly Val Ala Cys Asn Pro Ala Cys Phe Ile																				
370 375 380																				



245 250 255  
 Ala Gly Pro Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn  
 260 265 270  
 Phe Gly Leu Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala  
 275 280 285  
 Ile Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser  
 290 295 300  
 Pro Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn  
 305 310 315 320  
 Gln Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn  
 325 330 335  
 Phe Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala  
 340 345 350  
 Met Ile Asn Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala  
 355 360 365  
 Val Ala Ser Leu Gly Lys Gly Val Ala Cys Asn Pro Ala Cys Phe Ile  
 370 375 380  
 Thr Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr  
 385 390 395 400  
 Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu Gln  
 405 410 415  
 Leu Glu Asn Thr Met Gln Met Ser Leu Lys Asp Leu Leu Ser Glu Lys  
 420 425 430  
 Asp Glu Leu  
 435

<210> 7  
 <211> 1278  
 <212> DNA  
 <213> Homo sapiens  
  
 <220>  
 <221> CDS  
 <222> (1)...(1275)

<400> 7  
 atg cag ctg agg aac cca gaa cta cat ctg ggc tgc gcg ctt gcg ctt 48  
 Met Gln Leu Arg Asn Pro Glu Leu His Leu Gly Cys Ala Leu Ala Leu  
 1 5 10 15  
  
 cgc ttc ctg gcc ctc gtt tcc tgg gac atc cct ggg gct aga gca ctg 96  
 Arg Phe Leu Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu  
 20 25 30  
  
 gac aat gga ttg gca agg acg cct acc atg ggc tgg ctg cac tgg gag 144  
 Asp Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu  
 35 40 45  
  
 cgc ttc atg tgc aac ctt gac tgc cag gaa gag cca gat tcc tgc atc 192  
 Arg Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile  
 50 55 60  
  
 agt gag aag ctc ttc atg gag atg gca gag ctc atg gtc tca gaa ggc 240  
 Ser Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly





atc atg gct gct cct tta ttc atg tct aat gac ctc cga cac atc agc 912  
 Ile Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser  
 290 295 300

cct caa gcc aaa gct ctc ctt cag gat aag gac gta att gcc atc aat 960  
 Pro Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn  
 305 310 315 320

cag gac ccc ttg ggc aag caa ggg tac cag ctt aga cag gga gac aac 1008  
 Gln Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn  
 325 330 335

ttt gaa gtg tgg gaa cga cct ctc tca ggc tta gcc tgg gct gta gct 1056  
 Phe Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala  
 340 345 350

atg ata aac cgg cag gag att ggt gga cct cgc tct tat acc atc gca 1104  
 Met Ile Asn Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala  
 355 360 365

gtt gct tcc ctg ggt aaa gga gtg gcc tgt aat cct gcc tgc ttc atc 1152  
 Val Ala Ser Leu Gly Lys Gly Val Ala Cys Asn Pro Ala Cys Phe Ile  
 370 375 380

aca cag ctc ctc cct gtg aaa agg aag cta ggg ttc tat gaa tgg act 1200  
 Thr Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr  
 385 390 395 400

tca agg tta aga agt cac ata aat ccc aca ggc act gtt ttg ctt cag 1248  
 Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu Gln  
 405 410 415

cta gaa aac aca atg cag atg tct tta tga 1278  
 Leu Glu Asn Thr Met Gln Met Ser Leu  
 420 425

<210> 8  
 <211> 424  
 <212> PRT  
 <213> Homo sapiens

<400> 8  
 Gln Leu Arg Asn Pro Glu Leu His Leu Gly Cys Ala Leu Ala Leu Arg  
 1 5 10 15  
 Phe Leu Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu Asp  
 20 25 30  
 Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu Arg  
 35 40 45  
 Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile Ser  
 50 55 60  
 Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly Trp  
 65 70 75 80  
 Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met Ala





210	215	220	
cac tgg cga aat ttt gct gac att gat gat tcc tgg aaa agt ata aag			720
His Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys			
225	230	235	240
agt atc ttg gac tgg aca tct ttt aac cag gag aga att gtt gat gtt			768
Ser Ile Leu Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val			
	245	250	255
gct gga cca ggg ggt tgg aat gac cca gat atg tta gtg att ggc aac			816
Ala Gly Pro Gly Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn			
	260	265	270
ttt ggc ctc agc tgg aat cag caa gta act cag atg gcc ctc tgg gct			864
Phe Gly Leu Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala			
	275	280	285
atc atg gct gct cct tta ttc atg tct aat gac ctc cga cac atc agc			912
Ile Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser			
	290	295	300
cct caa gcc aaa gct ctc ctt cag gat aag gac gta att gcc atc aat			960
Pro Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn			
	305	310	315
cag gac ccc ttg ggc aag caa ggg tac cag ctt aga cag gga gac aac			1008
Gln Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn			
	325	330	335
ttt gaa gtg tgg gaa cga cct ctc tca ggc tta gcc tgg gct gta gct			1056
Phe Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala			
	340	345	350
atg ata aac cgg cag gag att ggt gga cct cgc tct tat acc atc gca			1104
Met Ile Asn Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala			
	355	360	365
gtt gct tcc ctg ggt aaa gga gtg gcc tgt aat cct gcc tgc ttc atc			1152
Val Ala Ser Leu Gly Lys Gly Val Ala Cys Asn Pro Ala Cys Phe Ile			
	370	375	380
aca cag ctc ctc cct gtg aaa agg aag cta ggg ttc tat gaa tgg act			1200
Thr Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr			
	385	390	400
tca agg tta aga agt cac ata aat ccc aca ggc act gtt ttg ctt cag			1248
Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu Gln			
	405	410	415
cta gaa aac aca atg cag atg tct tta tct gaa aag gac gaa tta tga			1296
Leu Glu Asn Thr Met Gln Met Ser Leu Ser Glu Lys Asp Glu Leu *			
	420	425	430

<210> 10  
 <211> 431  
 <212> PRT  
 <213> Homo sapiens

<400> 10

Met	Gln	Leu	Arg	Asn	Pro	Glu	Leu	His	Leu	Gly	Cys	Ala	Leu	Ala	Leu
1				5					10					15	
Arg	Phe	Leu	Ala	Leu	Val	Ser	Trp	Asp	Ile	Pro	Gly	Ala	Arg	Ala	Leu
		20						25					30		
Asp	Asn	Gly	Leu	Ala	Arg	Thr	Pro	Thr	Met	Gly	Trp	Leu	His	Trp	Glu
		35					40					45			
Arg	Phe	Met	Cys	Asn	Leu	Asp	Cys	Gln	Glu	Glu	Pro	Asp	Ser	Cys	Ile
		50				55					60				
Ser	Glu	Lys	Leu	Phe	Met	Glu	Met	Ala	Glu	Leu	Met	Val	Ser	Glu	Gly
65					70					75					80
Trp	Lys	Asp	Ala	Gly	Tyr	Glu	Tyr	Leu	Cys	Ile	Asp	Asp	Cys	Trp	Met
				85					90					95	
Ala	Pro	Gln	Arg	Asp	Ser	Glu	Gly	Arg	Leu	Gln	Ala	Asp	Pro	Gln	Arg
			100					105					110		
Phe	Pro	His	Gly	Ile	Arg	Gln	Leu	Ala	Asn	Tyr	Val	His	Ser	Lys	Gly
		115					120					125			
Leu	Lys	Leu	Gly	Ile	Tyr	Ala	Asp	Val	Gly	Asn	Lys	Thr	Cys	Ala	Gly
		130				135					140				
Phe	Pro	Gly	Ser	Phe	Gly	Tyr	Tyr	Asp	Ile	Asp	Ala	Gln	Thr	Phe	Ala
145					150					155					160
Asp	Trp	Gly	Val	Asp	Leu	Leu	Lys	Phe	Asp	Gly	Cys	Tyr	Cys	Asp	Ser
				165				170						175	
Leu	Glu	Asn	Leu	Ala	Asp	Gly	Tyr	Lys	His	Met	Ser	Leu	Ala	Leu	Asn
			180					185					190		
Arg	Thr	Gly	Arg	Ser	Ile	Val	Tyr	Ser	Cys	Glu	Trp	Pro	Leu	Tyr	Met
		195					200						205		
Trp	Pro	Phe	Gln	Lys	Pro	Asn	Tyr	Thr	Glu	Ile	Arg	Gln	Tyr	Cys	Asn
		210				215					220				
His	Trp	Arg	Asn	Phe	Ala	Asp	Ile	Asp	Asp	Ser	Trp	Lys	Ser	Ile	Lys
225					230					235					240
Ser	Ile	Leu	Asp	Trp	Thr	Ser	Phe	Asn	Gln	Glu	Arg	Ile	Val	Asp	Val
				245					250					255	
Ala	Gly	Pro	Gly	Gly	Trp	Asn	Asp	Pro	Asp	Met	Leu	Val	Ile	Gly	Asn
			260					265					270		
Phe	Gly	Leu	Ser	Trp	Asn	Gln	Gln	Val	Thr	Gln	Met	Ala	Leu	Trp	Ala
		275					280					285			
Ile	Met	Ala	Ala	Pro	Leu	Phe	Met	Ser	Asn	Asp	Leu	Arg	His	Ile	Ser
		290				295					300				
Pro	Gln	Ala	Lys	Ala	Leu	Leu	Gln	Asp	Lys	Asp	Val	Ile	Ala	Ile	Asn
305					310					315					320
Gln	Asp	Pro	Leu	Gly	Lys	Gln	Gly	Tyr	Gln	Leu	Arg	Gln	Gly	Asp	Asn
				325					330					335	
Phe	Glu	Val	Trp	Glu	Arg	Pro	Leu	Ser	Gly	Leu	Ala	Trp	Ala	Val	Ala
			340					345					350		
Met	Ile	Asn	Arg	Gln	Glu	Ile	Gly	Gly	Pro	Arg	Ser	Tyr	Thr	Ile	Ala
		355					360					365			
Val	Ala	Ser	Leu	Gly	Lys	Gly	Val	Ala	Cys	Asn	Pro	Ala	Cys	Phe	Ile

370		375		380
Thr Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr				
385		390		400
Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu Gln				
	405		410	415
Leu Glu Asn Thr Met Gln Met Ser Leu Ser Glu Lys Asp Glu Leu				
	420		425	430

<210> 11  
 <211> 1266  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(1266)

<400> 11

atg cag ctg agg aac cca gaa cta cat ctg ggc tgc gcg ctt gcg ctt	48
Met Gln Leu Arg Asn Pro Glu Leu His Leu Gly Cys Ala Leu Ala Leu	
1 5 10 15	
cgc ttc ctg gcc ctc gtt tcc tgg gac atc cct ggg gct aga gca ctg	96
Arg Phe Leu Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu	
20 25 30	
gac aat gga ttg gca agg acg cct acc atg ggc tgg ctg cac tgg gag	144
Asp Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu	
35 40 45	
cgc ttc atg tgc aac ctt gac tgc cag gaa gag cca gat tcc tgc atc	192
Arg Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile	
50 55 60	
agt gag aag ctc ttc atg gag atg gca gag ctc atg gtc tca gaa ggc	240
Ser Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly	
65 70 75 80	
tgg aag gat gca ggt tat gag tac ctc tgc att gat gac tgt tgg atg	288
Trp Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met	
85 90 95	
gct ccc caa aga gat tca gaa ggc aga ctt cag gca gac cct cag cgc	336
Ala Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg	
100 105 110	
ttt cct cat ggg att cgc cag cta gct aat tat gtt cac agc aaa gga	384
Phe Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly	
115 120 125	
ctg aag cta ggg att tat gca gat gtt gga aat aaa acc tgc gca ggc	432
Leu Lys Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly	
130 135 140	

100  
 90  
 80  
 70  
 60  
 50  
 40  
 30  
 20  
 10  
 0

ttc cct ggg agt ttt gga tac tac gac att gat gcc cag acc ttt gct Phe Pro Gly Ser Phe Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala 145 150 155 160	480
gac tgg gga gta gat ctg cta aaa ttt gat ggt tgt tac tgt gac agt Asp Trp Gly Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser 165 170 175	528
ttg gaa aat ttg gca gat ggt tat aag cac atg tcc ttg gcc ctg aat Leu Glu Asn Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn 180 185 190	576
agg act ggc aga agc att gtg tac tcc tgt gag tgg cct ctt tat atg Arg Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met 195 200 205	624
tgg ccc ttt caa aag ccc aat tat aca gaa atc cga cag tac tgc aat Trp Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn 210 215 220	672
cac tgg cga aat ttt gct gac att gat gat tcc tgg aaa agt ata aag His Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys 225 230 235 240	720
agt atc ttg gac tgg aca tct ttt aac cag gag aga att gtt gat gtt Ser Ile Leu Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val 245 250 255	768
gct gga cca ggg ggt tgg aat gac cca gat atg tta gtg att ggc aac Ala Gly Pro Gly Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn 260 265 270	816
ttt ggc ctc agc tgg aat cag caa gta act cag atg gcc ctc tgg gct Phe Gly Leu Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala 275 280 285	864
atc atg gct gct cct tta ttc atg tct aat gac ctc cga cac atc agc Ile Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser 290 295 300	912
cct caa gcc aaa gct ctc ctt cag gat aag gac gta att gcc atc aat Pro Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn 305 310 315 320	960
cag gac ccc ttg ggc aag caa ggg tac cag ctt aga cag gga gac aac Gln Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn 325 330 335	1008
ttt gaa gtg tgg gaa cga cct ctc tca ggc tta gcc tgg gct gta gct Phe Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala 340 345 350	1056
atg ata aac cgg cag gag att ggt gga cct cgc tct tat acc atc gca Met Ile Asn Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala	1104



355	360	365	
gtt gct tcc ctg ggt aaa gga gtg gcc tgt aat cct gcc tgc ttc atc			1152
Val Ala Ser Leu Gly Lys Gly Val Ala Cys Asn Pro Ala Cys Phe Ile			
370	375	380	
aca cag ctc ctc cct gtg aaa agg aag cta ggg ttc tat gaa tgg act			1200
Thr Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr			
385	390	395	400
tca agg tta aga agt cac ata aat ccc aca ggc act gtt ttg ctt cag			1248
Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu Gln			
405	410	415	
cta gaa aac aca atg taa			1266
Leu Glu Asn Thr Met *			
420			

<210> 12  
 <211> 421  
 <212> PRT  
 <213> Homo sapiens

<400> 12

Met	Gln	Leu	Arg	Asn	Pro	Glu	Leu	His	Leu	Gly	Cys	Ala	Leu	Ala	Leu
1				5					10				15		
Arg	Phe	Leu	Ala	Leu	Val	Ser	Trp	Asp	Ile	Pro	Gly	Ala	Arg	Ala	Leu
		20						25					30		
Asp	Asn	Gly	Leu	Ala	Arg	Thr	Pro	Thr	Met	Gly	Trp	Leu	His	Trp	Glu
	35						40					45			
Arg	Phe	Met	Cys	Asn	Leu	Asp	Cys	Gln	Glu	Glu	Pro	Asp	Ser	Cys	Ile
	50					55					60				
Ser	Glu	Lys	Leu	Phe	Met	Glu	Met	Ala	Glu	Leu	Met	Val	Ser	Glu	Gly
	65				70					75					80
Trp	Lys	Asp	Ala	Gly	Tyr	Glu	Tyr	Leu	Cys	Ile	Asp	Asp	Cys	Trp	Met
				85					90					95	
Ala	Pro	Gln	Arg	Asp	Ser	Glu	Gly	Arg	Leu	Gln	Ala	Asp	Pro	Gln	Arg
			100					105					110		
Phe	Pro	His	Gly	Ile	Arg	Gln	Leu	Ala	Asn	Tyr	Val	His	Ser	Lys	Gly
		115					120					125			
Leu	Lys	Leu	Gly	Ile	Tyr	Ala	Asp	Val	Gly	Asn	Lys	Thr	Cys	Ala	Gly
	130					135					140				
Phe	Pro	Gly	Ser	Phe	Gly	Tyr	Tyr	Asp	Ile	Asp	Ala	Gln	Thr	Phe	Ala
	145				150					155					160
Asp	Trp	Gly	Val	Asp	Leu	Leu	Lys	Phe	Asp	Gly	Cys	Tyr	Cys	Asp	Ser
				165					170					175	
Leu	Glu	Asn	Leu	Ala	Asp	Gly	Tyr	Lys	His	Met	Ser	Leu	Ala	Leu	Asn
		180						185					190		
Arg	Thr	Gly	Arg	Ser	Ile	Val	Tyr	Ser	Cys	Glu	Trp	Pro	Leu	Tyr	Met
	195						200					205			
Trp	Pro	Phe	Gln	Lys	Pro	Asn	Tyr	Thr	Glu	Ile	Arg	Gln	Tyr	Cys	Asn
	210					215					220				
His	Trp	Arg	Asn	Phe	Ala	Asp	Ile	Asp	Asp	Ser	Trp	Lys	Ser	Ile	Lys

```

225          230          235          240
Ser Ile Leu Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val
          245          250          255
Ala Gly Pro Gly Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn
          260          265          270
Phe Gly Leu Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala
          275          280          285
Ile Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser
          290          295          300
Pro Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn
305          310          315          320
Gln Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn
          325          330          335
Phe Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala
          340          345          350
Met Ile Asn Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala
          355          360          365
Val Ala Ser Leu Gly Lys Gly Val Ala Cys Asn Pro Ala Cys Phe Ile
          370          375          380
Thr Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr
385          390          395          400
Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu Gln
          405          410          415
Leu Glu Asn Thr Met
          420

```

```

<210> 13
<211> 1284
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (1)...(1284)

```

```

<400> 13
atg cag ctg agg aac cca gaa cta cat ctg ggc tgc gcg ctt gcg ctt      48
Met Gln Leu Arg Asn Pro Glu Leu His Leu Gly Cys Ala Leu Ala Leu
  1          5          10          15

cgc ttc ctg gcc ctc gtt tcc tgg gac atc cct ggg gct aga gca ctg      96
Arg Phe Leu Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu
          20          25          30

gac aat gga ttg gca agg acg cct acc atg ggc tgg ctg cac tgg gag     144
Asp Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu
          35          40          45

cgc ttc atg tgc aac ctt gac tgc cag gaa gag cca gat tcc tgc atc     192
Arg Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile
          50          55          60

agt gag aag ctc ttc atg gag atg gca gag ctc atg gtc tca gaa ggc     240
Ser Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly

```





```

      85              90              95
Ala Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg
      100              105              110
Phe Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly
      115              120              125
Leu Lys Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly
      130              135              140
Phe Pro Gly Ser Phe Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala
145              150              155              160
Asp Trp Gly Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser
      165              170              175
Leu Glu Asn Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn
      180              185              190
Arg Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met
      195              200              205
Trp Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn
      210              215              220
His Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys
225              230              235              240
Ser Ile Leu Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val
      245              250              255
Ala Gly Pro Gly Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn
      260              265              270
Phe Gly Leu Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala
      275              280              285
Ile Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser
      290              295              300
Pro Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn
305              310              315              320
Gln Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn
      325              330              335
Phe Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala
      340              345              350
Met Ile Asn Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala
      355              360              365
Val Ala Ser Leu Gly Lys Gly Val Ala Cys Asn Pro Ala Cys Phe Ile
      370              375              380
Thr Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr
385              390              395              400
Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu Gln
      405              410              415
Leu Glu Asn Thr Met Ser Glu Lys Asp Glu Leu
      420              425

```

<210> 15  
 <211> 1254  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(1254)

<400> 15

atg cag ctg agg aac cca gaa cta cat ctg ggc tgc gcg ctt gcg ctt	48
Met Gln Leu Arg Asn Pro Glu Leu His Leu Gly Cys Ala Leu Ala Leu	
1 5 10 15	
cgc ttc ctg gcc ctc gtt tcc tgg gac atc cct ggg gct aga gca ctg	96
Arg Phe Leu Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu	
20 25 30	
gac aat gga ttg gca agg acg cct acc atg ggc tgg ctg cac tgg gag	144
Asp Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu	
35 40 45	
cgc ttc atg tgc aac ctt gac tgc cag gaa gag cca gat tcc tgc atc	192
Arg Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile	
50 55 60	
agt gag aag ctc ttc atg gag atg gca gag ctc atg gtc tca gaa ggc	240
Ser Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly	
65 70 75 80	
tgg aag gat gca ggt tat gag tac ctc tgc att gat gac tgt tgg atg	288
Trp Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met	
85 90 95	
gct ccc caa aga gat tca gaa ggc aga ctt cag gca gac cct cag cgc	336
Ala Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg	
100 105 110	
ttt cct cat ggg att cgc cag cta gct aat tat gtt cac agc aaa gga	384
Phe Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly	
115 120 125	
ctg aag cta ggg att tat gca gat gtt gga aat aaa acc tgc gca ggc	432
Leu Lys Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly	
130 135 140	
ttc cct ggg agt ttt gga tac tac gac att gat gcc cag acc ttt gct	480
Phe Pro Gly Ser Phe Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala	
145 150 155 160	
gac tgg gga gta gat ctg cta aaa ttt gat ggt tgt tac tgt gac agt	528
Asp Trp Gly Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser	
165 170 175	
ttg gaa aat ttg gca gat ggt tat aag cac atg tcc ttg gcc ctg aat	576
Leu Glu Asn Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn	
180 185 190	
agg act ggc aga agc att gtg tac tcc tgt gag tgg cct ctt tat atg	624
Arg Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met	
195 200 205	
tgg ccc ttt caa aag ccc aat tat aca gaa atc cga cag tac tgc aat	672
Trp Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn	

210	215	220	
cac tgg cga aat ttt gct gac att gat gat tcc tgg aaa agt ata aag			720
His Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys			
225	230	235	240
agt atc ttg gac tgg aca tct ttt aac cag gag aga att gtt gat gtt			768
Ser Ile Leu Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val			
	245	250	255
gct gga cca ggg ggt tgg aat gac cca gat atg tta gtg att ggc aac			816
Ala Gly Pro Gly Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn			
	260	265	270
ttt ggc ctc agc tgg aat cag caa gta act cag atg gcc ctc tgg gct			864
Phe Gly Leu Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala			
	275	280	285
atc atg gct gct cct tta ttc atg tct aat gac ctc cga cac atc agc			912
Ile Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser			
	290	295	300
cct caa gcc aaa gct ctc ctt cag gat aag gac gta att gcc atc aat			960
Pro Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn			
305	310	315	320
cag gac ccc ttg ggc aag caa ggg tac cag ctt aga cag gga gac aac			1008
Gln Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn			
	325	330	335
ttt gaa gtg tgg gaa cga cct ctc tca ggc tta gcc tgg gct gta gct			1056
Phe Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala			
	340	345	350
atg ata aac cgg cag gag att ggt gga cct cgc tct tat acc atc gca			1104
Met Ile Asn Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala			
	355	360	365
gtt gct tcc ctg ggt aaa gga gtg gcc tgt aat cct gcc tgc ttc atc			1152
Val Ala Ser Leu Gly Lys Gly Val Ala Cys Asn Pro Ala Cys Phe Ile			
	370	375	380
aca cag ctc ctc cct gtg aaa agg aag cta ggg ttc tat gaa tgg act			1200
Thr Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr			
385	390	395	400
tca agg tta aga agt cac ata aat ccc aca ggc act gtt ttg ctt cag			1248
Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu Gln			
	405	410	415
cta taa			1254
Leu *			

<210> 16  
 <211> 417  
 <212> PRT  
 <213> Homo sapiens

<400> 16

Met	Gln	Leu	Arg	Asn	Pro	Glu	Leu	His	Leu	Gly	Cys	Ala	Leu	Ala	Leu
1				5					10					15	
Arg	Phe	Leu	Ala	Leu	Val	Ser	Trp	Asp	Ile	Pro	Gly	Ala	Arg	Ala	Leu
			20					25					30		
Asp	Asn	Gly	Leu	Ala	Arg	Thr	Pro	Thr	Met	Gly	Trp	Leu	His	Trp	Glu
		35					40					45			
Arg	Phe	Met	Cys	Asn	Leu	Asp	Cys	Gln	Glu	Glu	Pro	Asp	Ser	Cys	Ile
		50				55					60				
Ser	Glu	Lys	Leu	Phe	Met	Glu	Met	Ala	Glu	Leu	Met	Val	Ser	Glu	Gly
65					70					75					80
Trp	Lys	Asp	Ala	Gly	Tyr	Glu	Tyr	Leu	Cys	Ile	Asp	Asp	Cys	Trp	Met
				85					90					95	
Ala	Pro	Gln	Arg	Asp	Ser	Glu	Gly	Arg	Leu	Gln	Ala	Asp	Pro	Gln	Arg
			100					105					110		
Phe	Pro	His	Gly	Ile	Arg	Gln	Leu	Ala	Asn	Tyr	Val	His	Ser	Lys	Gly
		115					120					125			
Leu	Lys	Leu	Gly	Ile	Tyr	Ala	Asp	Val	Gly	Asn	Lys	Thr	Cys	Ala	Gly
		130				135					140				
Phe	Pro	Gly	Ser	Phe	Gly	Tyr	Tyr	Asp	Ile	Asp	Ala	Gln	Thr	Phe	Ala
145					150					155					160
Asp	Trp	Gly	Val	Asp	Leu	Leu	Lys	Phe	Asp	Gly	Cys	Tyr	Cys	Asp	Ser
				165					170					175	
Leu	Glu	Asn	Leu	Ala	Asp	Gly	Tyr	Lys	His	Met	Ser	Leu	Ala	Leu	Asn
		180						185					190		
Arg	Thr	Gly	Arg	Ser	Ile	Val	Tyr	Ser	Cys	Glu	Trp	Pro	Leu	Tyr	Met
		195					200					205			
Trp	Pro	Phe	Gln	Lys	Pro	Asn	Tyr	Thr	Glu	Ile	Arg	Gln	Tyr	Cys	Asn
		210				215						220			
His	Trp	Arg	Asn	Phe	Ala	Asp	Ile	Asp	Asp	Ser	Trp	Lys	Ser	Ile	Lys
225				230						235					240
Ser	Ile	Leu	Asp	Trp	Thr	Ser	Phe	Asn	Gln	Glu	Arg	Ile	Val	Asp	Val
			245						250					255	
Ala	Gly	Pro	Gly	Gly	Trp	Asn	Asp	Pro	Asp	Met	Leu	Val	Ile	Gly	Asn
			260					265					270		
Phe	Gly	Leu	Ser	Trp	Asn	Gln	Gln	Val	Thr	Gln	Met	Ala	Leu	Trp	Ala
		275					280					285			
Ile	Met	Ala	Ala	Pro	Leu	Phe	Met	Ser	Asn	Asp	Leu	Arg	His	Ile	Ser
	290					295					300				
Pro	Gln	Ala	Lys	Ala	Leu	Leu	Gln	Asp	Lys	Asp	Val	Ile	Ala	Ile	Asn
305					310					315					320
Gln	Asp	Pro	Leu	Gly	Lys	Gln	Gly	Tyr	Gln	Leu	Arg	Gln	Gly	Asp	Asn
			325						330					335	
Phe	Glu	Val	Trp	Glu	Arg	Pro	Leu	Ser	Gly	Leu	Ala	Trp	Ala	Val	Ala
			340					345					350		
Met	Ile	Asn	Arg	Gln	Glu	Ile	Gly	Gly	Pro	Arg	Ser	Tyr	Thr	Ile	Ala
		355					360					365			
Val	Ala	Ser	Leu	Gly	Lys	Gly	Val	Ala	Cys	Asn	Pro	Ala	Cys	Phe	Ile



370	375	380
Thr Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr		
385	390	395
Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu Gln		400
	405	410
		415
Leu		

<210> 17  
 <211> 1272  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(1272)

<400> 17

atg cag ctg agg aac cca gaa cta cat ctg ggc tgc gcg ctt gcg ctt	48
Met Gln Leu Arg Asn Pro Glu Leu His Leu Gly Cys Ala Leu Ala Leu	
1 5 10 15	
cgc ttc ctg gcc ctc gtt tcc tgg gac atc cct ggg gct aga gca ctg	96
Arg Phe Leu Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu	
20 25 30	
gac aat gga ttg gca agg acg cct acc atg ggc tgg ctg cac tgg gag	144
Asp Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu	
35 40 45	
cgc ttc atg tgc aac ctt gac tgc cag gaa gag cca gat tcc tgc atc	192
Arg Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile	
50 55 60	
agt gag aag ctc ttc atg gag atg gca gag ctc atg gtc tca gaa ggc	240
Ser Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly	
65 70 75 80	
tgg aag gat gca ggt tat gag tac ctc tgc att gat gac tgt tgg atg	288
Trp Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met	
85 90 95	
gct ccc caa aga gat tca gaa ggc aga ctt cag gca gac cct cag cgc	336
Ala Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg	
100 105 110	
ttt cct cat ggg att cgc cag cta gct aat tat gtt cac agc aaa gga	384
Phe Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly	
115 120 125	
ctg aag cta ggg att tat gca gat gtt gga aat aaa acc tgc gca ggc	432
Leu Lys Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly	
130 135 140	

ttc cct ggg agt ttt gga tac tac gac att gat gcc cag acc ttt gct	480
Phe Pro Gly Ser Phe Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala	
145 150 155 160	
gac tgg gga gta gat ctg cta aaa ttt gat ggt tgt tac tgt gac agt	528
Asp Trp Gly Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser	
165 170 175	
ttg gaa aat ttg gca gat ggt tat aag cac atg tcc ttg gcc ctg aat	576
Leu Glu Asn Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn	
180 185 190	
agg act ggc aga agc att gtg tac tcc tgt gag tgg cct ctt tat atg	624
Arg Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met	
195 200 205	
tgg ccc ttt caa aag ccc aat tat aca gaa atc cga cag tac tgc aat	672
Trp Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn	
210 215 220	
cac tgg cga aat ttt gct gac att gat gat tcc tgg aaa agt ata aag	720
His Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys	
225 230 235 240	
agt atc ttg gac tgg aca tct ttt aac cag gag aga att gtt gat gtt	768
Ser Ile Leu Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val	
245 250 255	
gct gga cca ggg ggt tgg aat gac cca gat atg tta gtg att ggc aac	816
Ala Gly Pro Gly Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn	
260 265 270	
ttt ggc ctc agc tgg aat cag caa gta act cag atg gcc ctc tgg gct	864
Phe Gly Leu Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala	
275 280 285	
atc atg gct gct cct tta ttc atg tct aat gac ctc cga cac atc agc	912
Ile Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser	
290 295 300	
cct caa gcc aaa gct ctc ctt cag gat aag gac gta att gcc atc aat	960
Pro Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn	
305 310 315 320	
cag gac ccc ttg ggc aag caa ggg tac cag ctt aga cag gga gac aac	1008
Gln Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn	
325 330 335	
ttt gaa gtg tgg gaa cga cct ctc tca ggc tta gcc tgg gct gta gct	1056
Phe Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Val Ala	
340 345 350	
atg ata aac cgg cag gag att ggt gga cct cgc tct tat acc atc gca	1104
Met Ile Asn Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala	

355	360	365	
gtt gct tcc ctg ggt aaa gga gtg gcc tgt aat cct gcc tgc ttc atc			1152
Val Ala Ser Leu Gly Lys Gly Val Ala Cys Asn Pro Ala Cys Phe Ile			
370	375	380	
aca cag ctc ctc cct gtg aaa agg aag cta ggg ttc tat gaa tgg act			1200
Thr Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr			
385	390	395	400
tca agg tta aga agt cac ata aat ccc aca ggc act gtt ttg ctt cag			1248
Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu Gln			
405	410	415	
cta tct gaa aag gac gaa tta tga			1272
Leu Ser Glu Lys Asp Glu Leu *			
420			

<210> 18  
 <211> 423  
 <212> PRT  
 <213> Homo sapiens  
 <400> 18  
 Met Gln Leu Arg Asn Pro Glu Leu His Leu Gly Cys Ala Leu Ala Leu  
 1 5 10 15  
 Arg Phe Leu Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu  
 20 25 30  
 Asp Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu  
 35 40 45  
 Arg Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile  
 50 55 60  
 Ser Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly  
 65 70 75 80  
 Trp Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met  
 85 90 95  
 Ala Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg  
 100 105 110  
 Phe Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly  
 115 120 125  
 Leu Lys Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly  
 130 135 140  
 Phe Pro Gly Ser Phe Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala  
 145 150 155 160  
 Asp Trp Gly Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser  
 165 170 175  
 Leu Glu Asn Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn  
 180 185 190  
 Arg Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met  
 195 200 205  
 Trp Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn  
 210 215 220  
 His Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys

1  
2  
3  
4  
5  
6  
7  
8  
9  
10  
11  
12  
13  
14  
15  
16  
17  
18  
19  
20  
21  
22  
23  
24  
25  
26  
27  
28  
29  
30  
31  
32  
33  
34  
35  
36  
37  
38  
39  
40  
41  
42  
43  
44  
45  
46  
47  
48  
49  
50  
51  
52  
53  
54  
55  
56  
57  
58  
59  
60  
61  
62  
63  
64  
65  
66  
67  
68  
69  
70  
71  
72  
73  
74  
75  
76  
77  
78  
79  
80  
81  
82  
83  
84  
85  
86  
87  
88  
89  
90  
91  
92  
93  
94  
95  
96  
97  
98  
99  
100  
101  
102  
103  
104  
105  
106  
107  
108  
109  
110  
111  
112  
113  
114  
115  
116  
117  
118  
119  
120  
121  
122  
123  
124  
125  
126  
127  
128  
129  
130  
131  
132  
133  
134  
135  
136  
137  
138  
139  
140  
141  
142  
143  
144  
145  
146  
147  
148  
149  
150  
151  
152  
153  
154  
155  
156  
157  
158  
159  
160  
161  
162  
163  
164  
165  
166  
167  
168  
169  
170  
171  
172  
173  
174  
175  
176  
177  
178  
179  
180  
181  
182  
183  
184  
185  
186  
187  
188  
189  
190  
191  
192  
193  
194  
195  
196  
197  
198  
199  
200  
201  
202  
203  
204  
205  
206  
207  
208  
209  
210  
211  
212  
213  
214  
215  
216  
217  
218  
219  
220  
221  
222  
223  
224  
225  
226  
227  
228  
229  
230  
231  
232  
233  
234  
235  
236  
237  
238  
239  
240  
241  
242  
243  
244  
245  
246  
247  
248  
249  
250  
251  
252  
253  
254  
255  
256  
257  
258  
259  
260  
261  
262  
263  
264  
265  
266  
267  
268  
269  
270  
271  
272  
273  
274  
275  
276  
277  
278  
279  
280  
281  
282  
283  
284  
285  
286  
287  
288  
289  
290  
291  
292  
293  
294  
295  
296  
297  
298  
299  
300  
301  
302  
303  
304  
305  
306  
307  
308  
309  
310  
311  
312  
313  
314  
315  
316  
317  
318  
319  
320  
321  
322  
323  
324  
325  
326  
327  
328  
329  
330  
331  
332  
333  
334  
335  
336  
337  
338  
339  
340  
341  
342  
343  
344  
345  
346  
347  
348  
349  
350  
351  
352  
353  
354  
355  
356  
357  
358  
359  
360  
361  
362  
363  
364  
365  
366  
367  
368  
369  
370  
371  
372  
373  
374  
375  
376  
377  
378  
379  
380  
381  
382  
383  
384  
385  
386  
387  
388  
389  
390  
391  
392  
393  
394  
395  
396  
397  
398  
399  
400  
401  
402  
403  
404  
405  
406  
407  
408  
409  
410  
411  
412  
413  
414  
415  
416  
417  
418  
419  
420  
421  
422  
423  
424  
425  
426  
427  
428  
429  
430  
431  
432  
433  
434  
435  
436  
437  
438  
439  
440  
441  
442  
443  
444  
445  
446  
447  
448  
449  
450  
451  
452  
453  
454  
455  
456  
457  
458  
459  
460  
461  
462  
463  
464  
465  
466  
467  
468  
469  
470  
471  
472  
473  
474  
475  
476  
477  
478  
479  
480  
481  
482  
483  
484  
485  
486  
487  
488  
489  
490  
491  
492  
493  
494  
495  
496  
497  
498  
499  
500  
501  
502  
503  
504  
505  
506  
507  
508  
509  
510  
511  
512  
513  
514  
515  
516  
517  
518  
519  
520  
521  
522  
523  
524  
525  
526  
527  
528  
529  
530  
531  
532  
533  
534  
535  
536  
537  
538  
539  
540  
541  
542  
543  
544  
545  
546  
547  
548  
549  
550  
551  
552  
553  
554  
555  
556  
557  
558  
559  
560  
561  
562  
563  
564  
565  
566  
567  
568  
569  
570  
571  
572  
573  
574  
575  
576  
577  
578  
579  
580  
581  
582  
583  
584  
585  
586  
587  
588  
589  
590  
591  
592  
593  
594  
595  
596  
597  
598  
599  
600  
601  
602  
603  
604  
605  
606  
607  
608  
609  
610  
611  
612  
613  
614  
615  
616  
617  
618  
619  
620  
621  
622  
623  
624  
625  
626  
627  
628  
629  
630  
631  
632  
633  
634  
635  
636  
637  
638  
639  
640  
641  
642  
643  
644  
645  
646  
647  
648  
649  
650  
651  
652  
653  
654  
655  
656  
657  
658  
659  
660  
661  
662  
663  
664  
665  
666  
667  
668  
669  
670  
671  
672  
673  
674  
675  
676  
677  
678  
679  
680  
681  
682  
683  
684  
685  
686  
687  
688  
689  
690  
691  
692  
693  
694  
695  
696  
697  
698  
699  
700  
701  
702  
703  
704  
705  
706  
707  
708  
709  
710  
711  
712  
713  
714  
715  
716  
717  
718  
719  
720  
721  
722  
723  
724  
725  
726  
727  
728  
729  
730  
731  
732  
733  
734  
735  
736  
737  
738  
739  
740  
741  
742  
743  
744  
745  
746  
747  
748  
749  
750  
751  
752  
753  
754  
755  
756  
757  
758  
759  
760  
761  
762  
763  
764  
765  
766  
767  
768  
769  
770  
771  
772  
773  
774  
775  
776  
777  
778  
779  
780  
781  
782  
783  
784  
785  
786  
787  
788  
789  
790  
791  
792  
793  
794  
795  
796  
797  
798  
799  
800  
801  
802  
803  
804  
805  
806  
807  
808  
809  
810  
811  
812  
813  
814  
815  
816  
817  
818  
819  
820  
821  
822  
823  
824  
825  
826  
827  
828  
829  
830  
831  
832  
833  
834  
835  
836  
837  
838  
839  
840  
841  
842  
843  
844  
845  
846  
847  
848  
849  
850  
851  
852  
853  
854  
855  
856  
857  
858  
859  
860  
861  
862  
863  
864  
865  
866  
867  
868  
869  
870  
871  
872  
873  
874  
875  
876  
877  
878  
879  
880  
881  
882  
883  
884  
885  
886  
887  
888  
889  
890  
891  
892  
893  
894  
895  
896  
897  
898  
899  
900  
901  
902  
903  
904  
905  
906  
907  
908  
909  
910  
911  
912  
913  
914  
915  
916  
917  
918  
919  
920  
921  
922  
923  
924  
925  
926  
927  
928  
929  
930  
931  
932  
933  
934  
935  
936  
937  
938  
939  
940  
941  
942  
943  
944  
945  
946  
947  
948  
949  
950  
951  
952  
953  
954  
955  
956  
957  
958  
959  
960  
961  
962  
963  
964  
965  
966  
967  
968  
969  
970  
971  
972  
973  
974  
975  
976  
977  
978  
979  
980  
981  
982  
983  
984  
985  
986  
987  
988  
989  
990  
991  
992  
993  
994  
995  
996  
997  
998  
999  
1000

```

225          230          235          240
Ser Ile Leu Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val
          245          250          255
Ala Gly Pro Gly Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn
          260          265          270
Phe Gly Leu Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala
          275          280          285
Ile Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser
          290          295          300
Pro Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn
305          310          315          320
Gln Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn
          325          330          335
Phe Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala
          340          345          350
Met Ile Asn Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala
          355          360          365
Val Ala Ser Leu Gly Lys Gly Val Ala Cys Asn Pro Ala Cys Phe Ile
          370          375          380
Thr Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr
385          390          395          400
Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu Gln
          405          410          415
Leu Ser Glu Lys Asp Glu Leu
          420

```

```

<210> 19
<211> 1215
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (10)...(1215)

```

```

<400> 19
atgcagctg agg aac cca gaa cta cat ctg ggc tgc gcg ctt gcg ctt cgc      51
      Arg Asn Pro Glu Leu His Leu Gly Cys Ala Leu Ala Leu Arg
          1          5          10

ttc ctg gcc ctc gtt tcc tgg gac atc cct ggg gct aga gca ctg gac      99
Phe Leu Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu Asp
    15          20          25          30

aat gga ttg gca agg acg cct acc atg ggc tgg ctg cac tgg gag cgc      147
Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu Arg
          35          40          45

ttc atg tgc aac ctt gac tgc cag gaa gag cca gat tcc tgc atc agt      195
Phe Met Cys Asn Leu Asp Cys Gln Glu Pro Asp Ser Cys Ile Ser
          50          55          60

gag aag ctc ttc atg gag atg gca gag ctc atg gtc tca gaa ggc tgg      243
Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly Trp

```

65	70	75	
aag gat gca ggt tat gag tac ctc tgc att gat gac tgt tgg atg gct Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met Ala 80 85 90			291
ccc caa aga gat tca gaa ggc aga ctt cag gca gac cct cag cgc ttt Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg Phe 95 100 105 110			339
cct cat ggg att cgc cag cta gct aat tat gtt cac agc aaa gga ctg Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly Leu 115 120 125			387
aag cta ggg att tat gca gat gtt gga aat aaa acc tgc gca ggc ttc Lys Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly Phe 130 135 140			435
cct ggg agt ttt gga tac tac gac att gat gcc cag acc ttt gct gac Pro Gly Ser Phe Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala Asp 145 150 155			483
tgg gga gta gat ctg cta aaa ttt gat ggt tgt tac tgt gac agt ttg Trp Gly Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser Leu 160 165 170			531
gaa aat ttg gca gat ggt tat aag cac atg tcc ttg gcc ctg aat agg Glu Asn Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn Arg 175 180 185 190			579
act ggc aga agc att gtg tac tcc tgt gag tgg cct ctt tat atg tgg Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met Trp 195 200 205			627
ccc ttt caa aag ccc aat tat aca gaa atc cga cag tac tgc aat cac Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn His 210 215 220			675
tgg cga aat ttt gct gac att gat gat tcc tgg aaa agt ata aag agt Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys Ser 225 230 235			723
atc ttg gac tgg aca tct ttt aac cag gag aga att gtt gat gtt gct Ile Leu Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val Ala 240 245 250			771
gga cca ggg ggt tgg aat gac cca gat atg tta gtg att ggc aac ttt Gly Pro Gly Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn Phe 255 260 265 270			819
ggc ctc agc tgg aat cag caa gta act cag atg gcc ctc tgg gct atc Gly Leu Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala Ile 275 280 285			867

atg gct gct cct tta ttc atg tct aat gac ctc cga cac atc agc cct	915
Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser Pro	
290 295 300	
caa gcc aaa gct ctc ctt cag gat aag gac gta att gcc atc aat cag	963
Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn Gln	
305 310 315	
gac ccc ttg ggc aag caa ggg tac cag ctt aga cag gga gac aac ttt	1011
Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn Phe	
320 325 330	
gaa gtg tgg gaa cga cct ctc tca ggc tta gcc tgg gct gta gct atg	1059
Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala Met	
335 340 345 350	
ata aac cgg cag gag att ggt gga cct cgc tct tat acc atc gca gtt	1107
Ile Asn Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala Val	
355 360 365	
gct tcc ctg ggt aaa gga gtg gcc tgt aat cct gcc tgc ttc atc aca	1155
Ala Ser Leu Gly Lys Gly Val Ala Cys Asn Pro Ala Cys Phe Ile Thr	
370 375 380	
cag ctc ctc cct gtg aaa agg aag cta ggg ttc tat gaa tgg act tca	1203
Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr Ser	
385 390 395	
agg tta aga taa	1215
Arg Leu Arg *	
400	

<210> 20  
 <211> 401  
 <212> PRT  
 <213> Homo sapiens

<400> 20  
 Arg Asn Pro Glu Leu His Leu Gly Cys Ala Leu Ala Leu Arg Phe Leu  
 1 5 10 15  
 Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu Asp Asn Gly  
 20 25 30  
 Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu Arg Phe Met  
 35 40 45  
 Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile Ser Glu Lys  
 50 55 60  
 Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly Trp Lys Asp  
 65 70 75 80  
 Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met Ala Pro Gln  
 85 90 95  
 Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg Phe Pro His  
 100 105 110  
 Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly Leu Lys Leu

	115		120		125
Gly	Ile Tyr Ala Asp Val	Gly Asn Lys Thr Cys	Ala Gly Phe Pro Gly		
130		135	140		
Ser	Phe Gly Tyr Tyr Asp	Ile Asp Ala Gln Thr	Phe Ala Asp Trp Gly		
145		150	155		160
Val	Asp Leu Leu Lys Phe	Asp Gly Cys Tyr Cys	Asp Ser Leu Glu Asn		
	165	170	175		
Leu	Ala Asp Gly Tyr Lys	His Met Ser Leu Ala	Leu Asn Arg Thr Gly		
	180	185	190		
Arg	Ser Ile Val Tyr Ser	Cys Glu Trp Pro Leu	Tyr Met Trp Pro Phe		
	195	200	205		
Gln	Lys Pro Asn Tyr Thr	Glu Ile Arg Gln Tyr	Cys Asn His Trp Arg		
210		215	220		
Asn	Phe Ala Asp Ile Asp	Asp Ser Trp Lys Ser	Ile Lys Ser Ile Leu		
225		230	235		240
Asp	Trp Thr Ser Phe Asn	Gln Glu Arg Ile Val	Asp Val Ala Gly Pro		
	245	250	255		
Gly	Gly Trp Asn Asp Pro	Asp Met Leu Val Ile	Gly Asn Phe Gly Leu		
	260	265	270		
Ser	Trp Asn Gln Gln Val	Thr Gln Met Ala Leu	Trp Ala Ile Met Ala		
	275	280	285		
Ala	Pro Leu Phe Met Ser	Asn Asp Leu Arg His	Ile Ser Pro Gln Ala		
	290	295	300		
Lys	Ala Leu Leu Gln Asp	Lys Asp Val Ile Ala	Ile Asn Gln Asp Pro		
305		310	315		320
Leu	Gly Lys Gln Gly Tyr	Gln Leu Arg Gln Gly	Asp Asn Phe Glu Val		
	325	330	335		
Trp	Glu Arg Pro Leu Ser	Gly Leu Ala Trp Ala	Val Ala Met Ile Asn		
	340	345	350		
Arg	Gln Glu Ile Gly Gly	Pro Arg Ser Tyr Thr	Ile Ala Val Ala Ser		
	355	360	365		
Leu	Gly Lys Gly Val Ala	Cys Asn Pro Ala Cys	Phe Ile Thr Gln Leu		
	370	375	380		
Leu	Pro Val Lys Arg Lys	Leu Gly Phe Tyr Glu	Trp Thr Ser Arg Leu		
385		390	395		400
Arg					

<210> 21  
 <211> 1233  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(1233)

<400> 21	
atg cag ctg agg aac cca gaa cta cat ctg ggc tgc gcg ctt gcg ctt	48
Met Gln Leu Arg Asn Pro Glu Leu His Leu Gly Cys Ala Leu Ala Leu	
1 5 10 15	

cgc ttc ctg gcc ctc gtt tcc tgg gac atc cct ggg gct aga gca ctg	96
Arg Phe Leu Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu	

	20	25	30	
	gac aat gga ttg gca agg acg cct acc atg ggc tgg ctg cac tgg gag			144
	Asp Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu			
	35	40	45	
	cgc ttc atg tgc aac ctt gac tgc cag gaa gag cca gat tcc tgc atc			192
	Arg Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile			
	50	55	60	
	agt gag aag ctc ttc atg gag atg gca gag ctc atg gtc tca gaa ggc			240
	Ser Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly			
	65	70	75	80
	tgg aag gat gca ggt tat gag tac ctc tgc att gat gac tgt tgg atg			288
	Trp Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met			
	85	90	95	
	gct ccc caa aga gat tca gaa ggc aga ctt cag gca gac cct cag cgc			336
	Ala Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg			
	100	105	110	
	ttt cct cat ggg att cgc cag cta gct aat tat gtt cac agc aaa gga			384
	Phe Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly			
	115	120	125	
	ctg aag cta ggg att tat gca gat gtt gga aat aaa acc tgc gca ggc			432
	Leu Lys Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly			
	130	135	140	
	ttc cct ggg agt ttt gga tac tac gac att gat gcc cag acc ttt gct			480
	Phe Pro Gly Ser Phe Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala			
	145	150	155	160
	gac tgg gga gta gat ctg cta aaa ttt gat ggt tgt tac tgt gac agt			528
	Asp Trp Gly Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser			
	165	170	175	
	ttg gaa aat ttg gca gat ggt tat aag cac atg tcc ttg gcc ctg aat			576
	Leu Glu Asn Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn			
	180	185	190	
	agg act ggc aga agc att gtg tac tcc tgt gag tgg cct ctt tat atg			624
	Arg Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met			
	195	200	205	
	tgg ccc ttt caa aag ccc aat tat aca gaa atc cga cag tac tgc aat			672
	Trp Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn			
	210	215	220	
	cac tgg cga aat ttt gct gac att gat gat tcc tgg aaa agt ata aag			720
	His Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys			
	225	230	235	240



```

agt atc ttg gac tgg aca tct ttt aac cag gag aga att gtt gat gtt 768
Ser Ile Leu Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val
      245              250              255

gct gga cca ggg ggt tgg aat gac cca gat atg tta gtg att ggc aac 816
Ala Gly Pro Gly Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn
      260              265              270

ttt ggc ctc agc tgg aat cag caa gta act cag atg gcc ctc tgg gct 864
Phe Gly Leu Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala
      275              280              285

atc atg gct gct cct tta ttc atg tct aat gac ctc cga cac atc agc 912
Ile Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser
      290              295              300

cct caa gcc aaa gct ctc ctt cag gat aag gac gta att gcc atc aat 960
Pro Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn
      305              310              315              320

cag gac ccc ttg ggc aag caa ggg tac cag ctt aga cag gga gac aac 1008
Gln Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn
      325              330              335

ttt gaa gtg tgg gaa cga cct ctc tca ggc tta gcc tgg gct gta gct 1056
Phe Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala
      340              345              350

atg ata aac cgg cag gag att ggt gga cct cgc tct tat acc atc gca 1104
Met Ile Asn Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala
      355              360              365

gtt gct tcc ctg ggt aaa gga gtg gcc tgt aat cct gcc tgc ttc atc 1152
Val Ala Ser Leu Gly Lys Gly Val Ala Cys Asn Pro Ala Cys Phe Ile
      370              375              380

aca cag ctc ctc cct gtg aaa agg aag cta ggg ttc tat gaa tgg act 1200
Thr Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr
      385              390              395              400

tca agg tta aga tct gaa aag gac gaa tta tga 1233
Ser Arg Leu Arg Ser Glu Lys Asp Glu Leu *
      405              410

```

```

<210> 22
<211> 409
<212> PRT
<213> Homo sapiens

```

```

<400> 22
Gln Leu Arg Asn Pro Glu Leu His Leu Gly Cys Ala Leu Ala Leu Arg
 1           5           10           15
Phe Leu Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu Asp

```

```

      20      25      30
Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu Arg
  35      40      45
Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile Ser
  50      55      60
Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly Trp
  65      70      75      80
Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met Ala
      85      90      95
Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg Phe
      100      105      110
Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly Leu
      115      120      125
Lys Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly Phe
      130      135      140
Pro Gly Ser Phe Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala Asp
      145      150      155      160
Trp Gly Val Asp Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser Leu
      165      170      175
Glu Asn Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn Arg
      180      185      190
Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met Trp
      195      200      205
Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn His
      210      215      220
Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys Ser
      225      230      235      240
Ile Leu Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val Ala
      245      250      255
Gly Pro Gly Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn Phe
      260      265      270
Gly Leu Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala Ile
      275      280      285
Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser Pro
      290      295      300
Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn Gln
      305      310      315      320
Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn Phe
      325      330      335
Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala Met
      340      345      350
Ile Asn Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala Val
      355      360      365
Ala Ser Leu Gly Lys Gly Val Ala Cys Asn Pro Ala Cys Phe Ile Thr
      370      375      380
Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr Ser
      385      390      395      400
Arg Leu Arg Ser Glu Lys Asp Glu Leu
      405

```

<210> 23

<211> 30

<212> PRT

<213> Tobacco mosaic virus

<400> 23

Thr Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu  
1 5 10 15  
Gln Leu Glu Asn Thr Met Gln Met Ser Leu Lys Asp Leu Leu  
20 25 30

<210> 24

<211> 36

<212> PRT

<213> Tobacco mosaic virus

<400> 24

Thr Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu  
1 5 10 15  
Gln Leu Glu Asn Thr Met Gln Met Ser Leu Lys Asp Leu Ser Glu  
20 25 30  
Lys Asp Glu Leu  
35

<210> 25

<211> 26

<212> PRT

<213> Tobacco mosaic virus

<400> 25

Thr Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu  
1 5 10 15  
Gln Leu Glu Asn Thr Met Gln Met Ser Leu  
20 25

<210> 26

<211> 32

<212> PRT

<213> Tobacco mosaic virus

<400> 26

Thr Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu  
1 5 10 15  
Gln Leu Glu Asn Thr Met Gln Met Ser Leu Ser Glu Lys Asp Glu Leu  
20 25 30

<210> 27

<211> 22

<212> PRT

<213> Tobacco mosaic virus

<400> 27

Thr Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu  
1 5 10 15  
Gln Leu Glu Asn Thr Met  
20

<210> 28

<211> 29  
 <212> PRT  
 <213> Tobacco mosaic virus

<400> 28  
 Thr Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Thr Val Leu  
 1 5 10 15  
 Leu Gln Leu Glu Asn Thr Met Ser Glu Lys Asp Glu Leu  
 20 25

<210> 29  
 <211> 18  
 <212> PRT  
 <213> Tobacco mosaic virus

<400> 29  
 Thr Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu  
 1 5 10 15  
 Gln Leu

<210> 30  
 <211> 24  
 <212> PRT  
 <213> Tobacco mosaic virus

<400> 30  
 Thr Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu  
 1 5 10 15  
 Gln Leu Ser Glu Lys Asp Glu Leu  
 20

<210> 31  
 <211> 5  
 <212> PRT  
 <213> Tobacco mosaic virus

<400> 31  
 Thr Ser Arg Leu Arg  
 1 5

<210> 32  
 <211> 11  
 <212> PRT  
 <213> Tobacco mosaic virus

<400> 32  
 Thr Ser Arg Leu Arg Ser Glu Lys Asp Glu Leu  
 1 5 10

<210> 33  
 <211> 11641  
 <212> DNA  
 <213> Tobacco mosaic virus

<400> 33

gtattttttac	aacaattacc	aacaacaaca	aacaacaaac	aacattacaa	ttactatttta	60
caattacaat	ggcatacaca	cagacagcta	ccacatcagc	tttgctggac	actgtccgag	120
gaaacaactc	cttggtcaat	gatctagcaa	agcgtcgtct	ttacgacaca	gcggttgaag	180
agtttaacgc	tcgtgaccgc	aggcccaagg	tgaacttttc	aaaagtaata	agcgaggagc	240
agacgcttat	tgctaccggg	gcgtatccag	aattccaaat	tacattttat	aacacgcaaa	300
atgccgtgca	ttcgcttgca	ggtggattgc	gatctttaga	actggaatat	ctgatgatgc	360
aaattcccta	cggatcattg	acttatgaca	taggcgggaa	ttttgcatcg	catctgttca	420
agggacgagc	atatgtacac	tgctgtatgc	ccaacctgga	cgttcgagac	atcatgcggc	480
acgaaggcca	gaaagacagt	attgaactat	acctttctag	gctagagaga	ggggggaaaa	540
cagtcccca	cttccaaaag	gaagcatttg	acagatacgc	agaaattcct	gaagacgctg	600
tctgtcacia	tactttccag	acaatgagac	atcagccgat	gcagcaatca	ggcagagtgt	660
atgccattgc	gctacacagc	atatatgaca	taccagccga	tgagttcggg	gcggcactct	720
tgaggaaaaa	tgctccatac	tgctatgccg	ctttccactt	ctctgagaac	ctgcttcttg	780
aagattcata	cgtcaatttg	gacgaaatca	acgcgtgttt	ttcgcgcgat	ggagacaagt	840
tgaccttttc	ttttgcatca	gagagtactc	ttaattattg	tcatagttat	tctaattattc	900
ttaagtatgt	gtgcaaaact	tacttcccgg	cctctaatag	agaggtttac	atgaaggagt	960
tttttagtcac	cagagttaat	acctgggttt	gtaagttttc	tagaatagat	actttttcttt	1020
tgtacaaaag	tgtggcccat	aaaagtgtag	atagtgcaga	gttttatact	gcaatggaag	1080
acgcatggca	ttacaaaaag	actcttgcaa	tgtgcaacag	cgagagaatc	ctccttgagg	1140
attcatcatc	agtcaattac	tggtttccca	aaatgaggga	tatggtcatc	gtaccattat	1200
tcgacatttc	tttgaggact	agtaagagga	cgcgcaaggga	agtcttagtg	tccaaggatt	1260
tcgtgtttac	agtgcctaac	cacattcgaa	cataccaggc	gaaagctctt	acatacgcaa	1320
atgtttttgtc	ctttgtcgaa	tcgattcgat	cgagggtaat	cattaacggg	gtgacagcga	1380
ggtccgaatg	ggatgtggac	aaatctttgt	tacaatcctt	gtccatgacg	ttttacctgc	1440
atactaagct	tgccgttcta	aaggatgact	tactgattag	caagttagtg	ctcgggttcga	1500
aaacgggtgtg	ccagcatgtg	tgggatgaga	tttcgctggc	gtttgggaac	gcatttccct	1560
ccgtgaaaga	gaggctcttg	aacaggaaac	ttatcagagt	ggcaggcgac	gcattagaga	1620
tcagggtgcc	tgatctatat	gtgaccttcc	acgacagatt	agtgactgag	tacaaggcct	1680
ctgtggacat	gcctgcgctt	gacattagga	agaagatgga	agaaacggaa	gtgatgtaca	1740
atgcactttc	agagttagcg	gtgttaaggg	agtctgacaa	attcgatgtt	gatgtttttt	1800
cccagatgtg	ccaatctttg	gaagttgacc	caatgacggc	agcgaagggt	atagtcgcgg	1860
tcgatgacaa	tgagagcggt	ctgactctca	catttgaacg	acctactgag	gcgaatgttg	1920
cgctagcttt	acaggtatcaa	gagaaggctt	cagaagggtc	tttggtagtt	acctcaagag	1980
aagttgaaga	accgtccatg	aagggttcga	tggccagagg	agagttacaa	ttagctgggtc	2040
ttgctggaga	tcacccggag	tcgtccctatt	ctaagaacga	ggagatagag	tcttttagagc	2100
agtttcataat	ggcaacggca	gattcggttaa	ttcgtaagca	gatgagctcg	attgtgtaca	2160
cgggtccgat	taaagttcag	caaatgaaaa	actttatcga	tagcctggta	gcatactat	2220
ctgctgcggt	gtcgaatctc	gtcaagatcc	tcaaagatac	agctgctatt	gaccttgaaa	2280
cccgtcaaaa	gtttggagtc	ttggatgttg	catctaggaa	gtggttaatc	aaaccaacgg	2340
ccaagagtca	tgcatggggt	gttggtgaaa	cccacgcgag	gaagtatcat	gtggcgcttt	2400
tgggaatatga	tgagcagggt	gtggtgacat	gcgatgattg	gagaagagta	gctgtcagct	2460
ctgagtctgt	tgtttattcc	gacatggcga	aactcagaac	tctgcgcaga	ctgcttcgaa	2520
acggagaacc	gcattgtcagt	agcgcaaagg	ttgttcttgt	ggacggagtt	ccgggctgtg	2580
ggaaaaccaa	agaaattctt	tccagggtta	attttgatga	agatctaatt	ttagtacctg	2640
ggaagcaagc	cgcggaaatg	atcagaagac	gtgcgaattc	ctcagggtat	attgtggcca	2700
cgaaggacaa	cgttaaaaacc	gttgattctt	tcattgatgaa	ttttgggaaa	agcacacgct	2760
gtcagttcaa	gagggttattc	attgatgaag	ggttgatgtt	gcatactggg	tgtgttaatt	2820
ttcttgtggc	gatgtcattg	tgcgaaattg	catatgttta	cggagacaca	cagcagattc	2880
catacatcaa	tagagtttca	ggattcccgt	accccgccca	ttttgccaaa	ttggaagttg	2940
acgaggtgga	gacacgcaga	actactctcc	gttgtccagc	cgatgtcaca	cattatctga	3000
acaggagata	tgagggtctt	gtcatgagca	cttcttcggt	taaaaagtct	gtttcgcagg	3060
agatgggtcgg	cggagccgcc	gtgatcaatc	cgatctcaaa	acccttgcac	ggcaagatcc	3120



gtactcctgt	gagtggcctc	tttatatgtg	gccctttcaa	aagcccaatt	atacagaaat	6420
ccgacagtac	tgcaatcact	ggcgaaat	tgctgacatt	gatgattcct	ggaaaagtat	6480
aaagagtatc	ttggactgga	catcttttaa	ccaggagaga	attgttgatg	ttgctggacc	6540
agggggttgg	aatgacccag	atatgttagt	gattggcaac	tttggcctca	gctggaatca	6600
gcaagtaact	cagatggccc	tctgggctat	catggctgct	cctttattca	tgtctaata	6660
cctccgacac	atcagccctc	aagccaaagc	tctccttcag	gataaggacg	taattgccat	6720
caatcaggac	cccttgggca	agcaagggtg	ccagcttaga	caggagagac	actttgaagt	6780
gtgggaacga	cctctctcag	gcttagcctg	ggctgtagct	atgataaacc	ggcaggagat	6840
tggtggacct	cgctcttata	ccatcgagct	tgcttccctg	ggtaaaggag	tggcctgtaa	6900
tcttgctgc	ttcatcacac	agctcctccc	tgtgaaaagg	aagctagggt	tctatgaatg	6960
gacttcaagg	ttaagaagtc	acataaatcc	cacaggcact	gttttgcttc	agctatctga	7020
aaaggacgaa	ttatgacctg	ggctcgcaaa	gtttcgaaac	aaatcctcaa	aaagaggtcc	7080
gaaaaataat	aataat	gtgagggg	ttcaggcgga	aggcctaaac	caaaaagt	7140
tgatgaagtt	gaaaaagagt	ttgataat	gattgaagat	gaagccgaga	cgctcggtcgc	7200
ggattctgat	tcgtattaaa	tatgtcttac	tcaatcactt	ctccatcgca	at	7260
ttgtcatctg	tatgggctga	ccctatagaa	ttgttaaacy	tttgtacaaa	ttcgttaggt	7320
aaccagtttc	aaacacagca	agcaagaact	actgttcaac	agcagttcag	cgaggtgtgg	7380
aaacctttcc	ctcagagcac	cgctcagatt	cctggcgatg	tttataaggt	gtacaggtac	7440
aatgcagttt	tagatcctct	aattactgcg	ttgctggggg	cttttgatac	taggaataga	7500
ataatcgaag	tagaaaacca	gcagagtc	acaacagctg	aaacgttaga	tgctaccgcg	7560
agggtagacg	acgctacggt	tgcaattcgg	tctgctataa	ataat	taatgaacta	7620
gtaagaggtg	ctggactgta	caatcagaat	acttttgaaa	gtatgtctgg	gttggtctgg	7680
acctctgcac	ctgcatctta	aatgcatagg	tgctgaaata	taaagt	gtttctaaaa	7740
cacacgtggt	acgtacgata	acgtacagtg	tttttccctc	cacttaaatc	gaagggtagt	7800
gtcttggagc	gcgcggagta	aacatatatg	gttcataat	gtccgtaggc	acgtaaaaaa	7860
agcgagggat	tcgaattccc	ccggaacccc	cggttggggc	ccaggtacca	attcttgaag	7920
acgaaagggc	ctcgtgatac	gcctat	ataggttaat	gtcatgataa	taatggtttc	7980
ttagacgtca	ggtggcactt	ttcggggaaa	tgtgcgcgga	acccctat	gtttat	8040
ctaaatacat	tcaaatatgt	atccgctcat	gagacaataa	ccctgataaa	tgcttcaata	8100
atattgaaaa	aggaagagta	tgagtattca	acatttccgt	gtcgccctta	ttcccttttt	8160
tgccgcattt	tgccctcctg	tttttgcctc	cccagaaacy	ctggtgaaag	taaaagatgc	8220
tgaagatcag	ttgggtgcac	gagtggtgta	catcgaactg	gatctcaaca	gcggtaagat	8280
ccttgagagt	tttcgccc	aagaacgttt	tccaatgatg	agcactttta	aagttctgct	8340
atgtggcgcg	gtattatccc	gtgttgacgc	cgggcaagag	caactcggtc	gccgcataca	8400
ctattctcag	aatgacttgg	ttgagtactc	accagtcaca	gaaaagcatc	ttacggatgg	8460
catgacagta	agagaattat	gcagtgctgc	cataaccatg	agtataaaca	ctgcggccaa	8520
cttacttctg	acaacgatcg	gaggaccgaa	ggagctaacc	gcttttttgc	acaacatggg	8580
ggatcatgta	actcgcttg	atcgttggga	accggagctg	aatgaagcca	taccaaacga	8640
cgagcgtgac	accacgatgc	ctgcagcaat	ggcaacaacy	ttgcgcaaac	tattaactgg	8700
cgaactactt	actctagctt	cccggcaaca	attaatagac	tggatggagg	cggtataaagt	8760
tgcaggacca	cttctgcgct	cggcccttcc	ggctggctgg	tttattgctg	ataaatctgg	8820
agccgggtgag	cgtgggtctc	gcggtatcat	tgcagcactg	gggccagatg	gtaagccctc	8880
ccgtatcgta	gttatctaca	cgacggggag	tcaggcaact	atggatgaac	gaaatagaca	8940
gatcgctgag	ataggtgcct	cactgattaa	gcattgggtg	ctgtcagacc	aagtttactc	9000
atatatactt	tagattgatt	taaaacttca	tttttaattt	aaaaggatct	aggtgaagat	9060
cctttttgat	aatctcatga	ccaaaatccc	ttaacgtgag	ttttcgttcc	actgagcgtc	9120
agaccccgta	gaaaagatca	aaggatcttc	ttgagatcct	ttttttctgc	gcgtaatctg	9180
ctgcttgcaa	acaaaaaac	caccgctacc	agcgggtggt	tgtttgccgg	atcaagagct	9240
accaactctt	tttccgaagg	taactggctt	cagcagagcg	cagataccaa	atactgtcct	9300
tctagtgtag	ccgtagttag	gccaccactt	caagaactct	gtagcaccgc	ctacatacct	9360
cgctctgcta	atcctgttac	cagtggctgc	tgccagtggc	gataagtcgt	gtcttaccgg	9420
gttggactca	agacgatagt	taccggataa	ggcgcagcgg	tcgggctgaa	cggggggttc	9480
gtgcacacag	cccagcttgg	agcgaacgac	ctacaccgaa	ctgagatacc	tacagcgtga	9540
gctatgagaa	agcggcacgc	ttcccgaagg	gagaaaggcg	gacaggtatc	cggtaaagcg	9600

```

caggggtcggga acaggagagc gcacgagggga gcttccaggg ggaaacgcct ggtatcttta 9660
tagtcctgtc ggggttcgcc acctctgact tgagcgtcga tttttgtgat gctcgtcagg 9720
ggggcgggagc ctatggaaaa acgccagcaa cggggccttt ttacggttcc tggccttttg 9780
ctggcctttt gctcacatgt tctttcctgc gttatccctt gattctgtgg ataaccgtat 9840
taccgccttt gagtgagctg ataccgctcg ccgcagccga acgaccgagc gcagcagatc 9900
agtgagcgag gaagcggaag agcgctgat gcggtatttt ctcttacgc atctgtgcgg 9960
tatttcacac cgcataatgt gcaactcag tacaatctgc tctgatgccg catagttaag 10020
ccagtataca ctccgctatc gctacgtgac tgggtcatgg ctgcgccccg acaccgccca 10080
acaccgctg acgcgcctg acgggcttgt ctgctcccg catccgctta cagacaagct 10140
gtgaccgtct cggggagctg catgtgtcag aggttttcac cgtcatcacc gaaacgcgcg 10200
aggcagctgc ggtaaagctc atcagcgtgg tcgtgaagcg attcacagat gtctgcctgt 10260
tcatccgcgt ccagctcggt gagtttctcc agaagcgtaa atgtctggct tctgataaag 10320
cgggccatgt taagggcggt tttttcctgt ttggctactt gatgcctccg tgtaaggggg 10380
aatttctgtt catgggggta atgataccga tgaaacgaga gaggatgctc acgatacggg 10440
ttactgatga tgaacatgcc cggttactgg aacgttgtga gggtaaacia ctggcggtat 10500
ggatgcggcg ggaccagaga aaaatcactc aggggtcaatg ccagcgcttc gttaatacag 10560
atgtagggtg tccacagggt agccagcagc atcctgcgat gcagatccgg aacataatgg 10620
tgcagggcgc tgacttcgcg gtttccagac ttacgaaac acggaaaccg aagaccattc 10680
atgttggtgc tcaggtcgca gacgttttgc agcagcagtc gcttcacgtt cgtcgcgta 10740
tcgggtgattc attctgctaa ccagtaaggc aaccccgcca gcctagccgg gtccctcaacg 10800
acaggagcac gatcatgcgc acccgtaggc aggaaccaac gctgcccag atgcgcgcg 10860
tgccgctgct ggagatggcg gacgcgatgg atatgttctg ccaagggttg gtttgcgcat 10920
tcacagttct ccgcaagaat tgattggctc caattcttgg agtggatgaat ccgttagcga 10980
ggtgcgcgcg gcttccattc aggtcgaggt ggcccggctc catgcaccgc gacgcaacgc 11040
ggggaggcag acaaggtata gggcggcgc tacaatccat gccaaaccgt tccatgtgct 11100
cgccgaggcg gcataaatcg ccgtgacgat cagcgggtcca gtgatcgaag ttaggctggg 11160
aagagccgcg agcgtatcct gaagctgtcc ctgatggctg tcatctacct gcctggacag 11220
catggcctgc aacgcgggca tcccgatgcc gccggaagcg agaagaatca taatggggaa 11280
ggccatccag cctcgcgtcg cgaacgccag caagacgtag cccagcgcgt cggccgccat 11340
gccggcgata atggcctgct tctcgcggaa acgtttgggt gcgggaccag tgacgaaggc 11400
ttgagcgagg gcgtgcaaga ttccgaatac cgcaagcgac aggcggatca tcgtcgcgct 11460
ccagcgaaag cggctcctcg cgaaaatgac ccagagcgct gccggcacct gtccctacgag 11520
ttgcatgata aagaagacag tcataagtgc ggcgacgata gtcatgcccc gcgcccaccg 11580
gaaggagctg actgggttga aggctctcaa gggcatcggt cgagatttag gtgacactat 11640
a

```

```

<210> 34
<211> 8234
<212> DNA
<213> Tobacco mosaic virus

```

```

<400> 34
gtatttttac aacaattacc aacaacaaca aacaacagac aacattacaa ttactattta 60
caattacaat ggcatacaca cagacagcta ccacatcagc tttgctggac actgtccgag 120
gaaacaactc cttgggtcaat gatctagcaa agcgtcgtct ttacgacaca gcggttgaag 180
agtttaacgc tcgtgaccgc agggcccaagg tgaacttttc aaaagtaata agcgaggagc 240
agacgcttat tgctaccggc gcgtatccag aattccaaat tacattttat aacacgcaa 300
atgccgtgca ttcgcttgca ggtggattgc gatctttaga actggaatat ctgatgatgc 360
aaattcccta cggatcattg acttatgaca taggcgggaa ttttgcacg catctgttca 420
agggacgagc atatgtacac tgctgcatgc ccaacctgga cgttcgagac atcatgcggc 480
acgaaggcca gaaagacagt attgaactat acctttctag gctagagaga ggggggaaaa 540
cagtccccaa cttccaaaag gaagcatttg acagatacgc agaaattcct gaagacgctg 600

```



tctgtcacaa	tactttccag	acatgcgaac	atcagccgat	gcagcaatca	ggcagagtgt	660
atgccattgc	gctacacagc	atatatgaca	taccagccga	tgagttcggg	gcggcactct	720
tgaggaaaaa	tgccatacgc	tgctatgccg	ctttccactt	ctccgagaac	ctgcttcttg	780
aagattcatg	cgtcaatttg	gacgaaatca	acgcgtgttt	ttcgcgcgat	ggagacaagt	840
tgaccttttc	ttttgcatca	gagagtactc	ttaattactg	tcatagttat	tctaattatc	900
ttaagtatgt	gtgcaaaaact	tacttcccgg	cctctaatag	agaggtttac	atgaaggagt	960
ttttagtcac	cagagttaat	acctggtttt	gtaagttttc	tagaatagat	acttttcttt	1020
tgtacaaaagg	tgtggcccat	aaaagtgtag	atagtgcgca	gttttatact	gcaatggaag	1080
acgcatggca	ttacaaaaag	actcttgcaa	tgtgcaacag	cgagagaatc	ctccttgggg	1140
attcatcatc	agtcaattac	tggtttccca	aaatgaggga	tatggtcac	gtaccattat	1200
tcgacatttc	tttggagact	agtaagagga	cgcgcaagga	agtcttagtg	tccaaggatt	1260
tcgtgttcac	agtgtttaac	cacattcgaa	cataccaggc	gaaagctctt	acatacgcaa	1320
atgttttgtc	cttcgtcgaa	tcgattcgat	cgagggtaat	cattaacggt	gtgacagcga	1380
gggtccgaatg	ggatgtggac	aaatctttgt	tacaatcctt	gtccatgacg	ttttacctgc	1440
atactaagct	tgccgttcta	aaggatgact	tactgattag	caagtttagt	ctcggttcga	1500
aaacggtgtg	ccagcatgtg	tgggatgaga	tttcgctggc	gtttgggaac	gcatttccct	1560
ccgtgaaaaga	gaggctcttg	aacaggaaaac	ttatcagagt	ggcaggcgac	gcattagaga	1620
tcagggtgcc	tgatctatat	gtgaccttcc	acgacagatt	agtgactgag	tacaaggcct	1680
ctgtggacat	gcctgcgctt	gacattagga	agaagatgga	agaaacggaa	gtgatgtaca	1740
atgcactttc	agaattatcg	gtgttaaggg	agtctgacaa	attcgatggt	gatgtttttt	1800
cccagatgtg	ccaatctttg	gaagttgacc	caatgacggc	agcgaagggt	atagtcgcgg	1860
tcatgagcaa	tgagagcggg	ctgactctca	catttgaacg	acctactgag	gcgaatgttg	1920
cgtagctttt	acaggatcaa	gagaaggctt	cagaagggtg	attggtagtt	acctcaagag	1980
aaagttgaaga	accgtccatg	aagggttcga	tggccagagg	agagttacaa	ttagctggtc	2040
ttgtctggaga	tcatccggaa	tcgtcctatt	ctaagaacga	ggagatagag	tcttttagagc	2100
agtttcatat	ggcgacggca	gattcgttaa	ttcgtaagca	gatgagctcg	atttgtgtaca	2160
cgggtccgat	taaagttcag	caaatgaaaa	actttatcga	tagcctggta	gcactactat	2220
ctgctgcggg	gtcgaatctc	gtcaagatcc	tcaaagatac	agctgctatt	gaccttgaaa	2280
cccgtcaaaa	gtttggagtc	ttggatgttg	catctaggaa	gtggttaatc	aaaccaacgg	2340
ccaagagtca	tgcatggggg	gttgttgaaa	cccacgcgag	ggagtatcat	gtggcgcttt	2400
tggaatatga	tgagcagggg	gtggtgacat	gcgatgattg	gagaagagta	gctgttagct	2460
ctgagtcctg	tgttttattcc	gacatggcga	aactcagaac	tctgcgcaga	ctgcttcgaa	2520
acgggagaacc	gcatgtcagt	agcgcaaaag	ttgttcttgt	ggacggagtt	ccgggctgtg	2580
gaaaaaccaa	agaaattctt	tccagggtta	atthttgatga	agatctaatt	ttagtacctg	2640
ggaagcaagc	cgcggaatg	atcagaagac	gtgcgaattc	ctcagggtt	attgtggcca	2700
cgaaggacaa	cgttaaaacc	gttgattctt	tcatgatgaa	ttttgggaaa	agcacacgct	2760
gtcagttcaa	gaggttattc	attgatgaag	ggttgatggt	gcatactggt	tgtgttaatt	2820
ttcttgtggc	gatgtcattg	tgcgaaattg	catatgttta	cggagacaca	cagcagattc	2880
catacatcaa	tagagtttca	ggattcccgt	accccgccca	ttttgccaaa	ttggaagttg	2940
acgaggtgga	gacacgcaga	actactctcc	gttgtccagc	cgatgtcaca	cattatctga	3000
acaggagata	tgagggtctt	gtcatgagca	cttcttcggg	taaaaagtct	gtttcgcagg	3060
agatggtcgg	cggagccgcc	gtgatcaatc	cgatctcaaa	acccttgcat	ggcaagatcc	3120
tgactttttac	ccaatcggat	aaagaagctc	tgctttcaag	agggtattca	gatgttcaca	3180
ctgtgcatga	agtgcaggc	gagacatact	ctgatgtttc	actagttagg	ttaaccctta	3240
caccggtctc	catcattgca	ggagacagcc	cacatgtttt	ggtcgcattg	tcaaggcaca	3300
cctgttcgct	caagtactac	actgttggtta	tggatccttt	agttagtatc	attagagatc	3360
tagagaaaact	tagctcgtac	ttgttagata	tgtataagg	cgatgcagga	acacaatagc	3420
aattacagat	tgactcgggtg	ttcaaagggt	ccaatctttt	tggtgcagcg	ccaaagactg	3480
gtgatatttc	tgatatgcag	ttttactatg	ataagtgtct	cccaggcaac	agcaccatga	3540
tgaataattt	tgatgctgtt	accatgagg	tgactgacat	ttcattgaat	gtcaaagatt	3600
gcatattgga	tatgtctaag	tctgttgctg	cacctaaagga	tcaaatcaaa	ccactaatat	3660
ctatggtacg	aacggcggca	gaaatgccac	gccagactgg	actattggaa	aatttagtgg	3720
cgatgattaa	aagaaacttt	aacgcacccg	agttgtctgg	catcattgat	attgaaaata	3780
ctgcatcttt	ggttgtagat	aagttttttg	atagttattt	gcttaaagaa	aaaagaaaac	3840

caaataaaaa	tgtttctttg	ttcagtagag	agtctctcaa	tagatgggta	gaaaagcagg	3900
aacaggtaac	aataggccag	ctcgcagatt	ttgattttgt	ggatttgcca	gcagttgatc	3960
agtacagaca	catgattaaa	gcacaaccca	aacaaaagtt	ggacacttca	atccaaacgg	4020
agtaccggc	tttgacagcg	attgtgtacc	attcaaaaaa	gatcaatgca	atattcggcc	4080
cgttgtttag	tgagcttact	aggcaattac	tggacagtgt	tgattcgagc	agatttttgt	4140
ttttcacaag	aaagacacca	gcgcagattg	aggattttct	cggagatctc	gacagtcacg	4200
tgccgatgga	tgtcttgagg	ctggatatat	caaaatacga	caaattctcag	aatgaattcc	4260
actgtgcagt	agaatacgag	atctggcgaa	gattgggttt	cgaagacttc	ttgggagaag	4320
tttggaacaa	agggcataga	aagaccaccc	tcaaggatta	taccgcaggt	ataaaaaact	4380
gcactctggta	tcaaagaaag	agcggggacg	tcacgacgtt	catttgaaac	actgtgatca	4440
ttgctgcatg	tttggcctcg	atgcttccga	tggagaaaat	aatcaaagga	gccttttgcg	4500
gtgacgatag	tctgctgtac	tttccaaagg	gttggtgagtt	tccggatgtg	caacactccg	4560
cgaatcttat	gtggaatttt	gaagcaaaac	tgtttaaaaa	acagtatgga	tacttttgcg	4620
gaagatatgt	aatacatcac	gacagaggat	gcattgtgta	ttacgatccc	ctaaagtga	4680
tctcgaaact	tggtgctaaa	cacatcaagg	attgggaaca	cttggaggag	ttcagaaggt	4740
ctctttgtga	tgttgctggt	tcgttgaaca	attgtgcgta	ttacacacag	ttggacgacg	4800
ctgtatggga	ggttcataag	accgcccctc	caggttcggt	tgtttataaa	agtctggtga	4860
agtatttgtc	tgataaagtt	cttttttagaa	gtttgtttat	agatggctct	agttgtttaa	4920
ggaaaagtga	atatcaatga	gtttatcgac	ctgacaaaaa	tggagaagat	cttaccgtcg	4980
atgtttaccc	ctgtaaagag	tgttatgtgt	tccaaagtgt	ataaaataat	ggttcatgag	5040
aatgagtcac	tgtaggggtg	gaaccttctt	aaaggagtta	agcttattga	tagtggatac	5100
gtctgtttag	ccggtttggt	cgtcacgggg	gagtggaaact	tgccctgaca	ttgcagagga	5160
gggtgtgagcg	tggtgctggt	ggacaaaaag	atggaaaagag	ccgacgaggg	cattctcgga	5220
tcttactaca	cagcagctgc	aaagaaaaga	tttcagttca	aggctggttc	caattatgct	5280
ataaccaccc	aggacgcat	gagaaacgtc	tggcaagttt	tagttaatat	tagaaatgtg	5340
aagatgtcag	cggttttctg	tccgctttct	ctggagtttg	tgctcggtgtg	tattgtttat	5400
agaaataata	taaaattagg	tttgagagag	aagattacaa	acgtgagaga	cggagggccc	5460
atggaactta	cagaagaagt	cgttgatgag	ttcatggaag	atgtccctat	gtcgatcagg	5520
cttgcaaatg	ttcgatctcg	aaccggaaaa	aagagtgatg	tccgcaaagg	gaaaaatagt	5580
agtagtgatc	ggtcagtgcc	gaacaagaac	tatagaaatg	ttaaggattt	tggaggaatg	5640
agttttaaaa	agaataatgt	aatcgatgat	gattcggagg	ctactgtcgc	cgaatcggat	5700
tcgttttaaa	tagatcttac	agtatcacta	ctccatctca	gttcgtgttc	ttgtcattaa	5760
ttaaaatgca	gctgaggaac	ccagaactac	atctgggctg	cgcgcttgcg	cttcgcttcc	5820
tggccctcgt	ttcctgggac	atccctgggg	ctagagcact	ggacaatgga	ttggcaagga	5880
cgcctaccat	gggctggctg	cactggggagc	gcttcatgtg	caaccttgac	tgccaggaag	5940
agccagattc	ctgcatcagt	gagaagctct	tcatggagat	ggcagagctc	atggctctcag	6000
aaggctggaa	ggatgcaggt	tatgagtacc	tctgcattga	tgactgttgg	atggctcccc	6060
aaagagattc	agaaggcaga	cttcaggcag	accctcagcg	ctttcctcat	gggattcgcc	6120
agctagctaa	ttatgttcac	agcaaggac	tgaagctagg	gatttatgca	gatgttggaa	6180
ataaaaacctg	cgcaggcttc	cctggggagt	ttggatacta	cgacattgat	gccagacct	6240
ttgctgactg	gggagtagat	ctgctaaaaa	ttgatgggtg	ttactgtgac	agtttggaag	6300
atttggcaga	tggttataag	cacatgtcct	tggccctgaa	taggactggc	agaagcattg	6360
tgtactcctg	tgagtggcct	ctttatatgt	ggccctttca	aaagcccaat	tatacagaaa	6420
tccgacagta	ctgcaatcac	tggcgaaaat	ttgctgacat	tgatgattcc	tggaaaagta	6480
taaagagtat	cttggactgg	acatctttta	accaggagag	aattgttgat	gttgctggac	6540
caggggggtg	gaatgaccca	gatatgttag	tgattggcaa	ctttggcctc	agctggaatc	6600
agcaagtaac	tcagatggcc	ctctgggcta	tcatggctgc	tcctttattc	atgtctaagt	6660
acctccgaca	catcagccct	caagccaaag	ctctccttca	ggataaggac	gtaattgccg	6720
tcaatcagga	ccccttgggc	aagcaagggt	accagcttag	acagggagac	aactttgaag	6780
tgtgggaacg	acctctctca	ggcttagcct	gggctgtagc	tatgataaac	cggcaggaga	6840
ttggtggacc	tcgctcttat	accatcgcat	ttgcttccct	gggtaaaagga	gtggcctgta	6900
atcctgcctg	cttcatcaca	cagctcctcc	ctgtgaaaag	gaagctaggg	ttctatgaat	6960
ggacttcaag	gttaagaagt	cacataaatc	ccacaggcac	tgttttgctt	cagctatctg	7020
aaaaggacga	attatgacct	agggggtagt	caagatgcat	aataaataac	ggatttgtgc	7080

